

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 1, 2005, 06:51:10 ; Search time 39 Seconds
(without alignments)
24.671 Million cell updates/sec

Title: US-10-780-321-13

Perfect score: 29

Sequence: 1 RXXXXXXGY 10

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	34	2 F82394	hypothetical prote
2	29	100.0	58	2 S34045	protamine - North
3	29	100.0	60	2 E90041	hypothetical prote
4	29	100.0	62	1 SBHUP	statherin precursor
5	29	100.0	63	2 H72737	probable ribosomal
6	29	100.0	71	2 AG1232	transcription regu
7	29	100.0	77	2 D69010	hypothetical prote
8	29	100.0	77	2 S68955	polyphenolic adhes
9	29	100.0	82	2 S00265	dipterocin A - nes
10	29	100.0	88	2 T36233	hypothetical prote
11	29	100.0	89	2 G64381	ribosomal protein
12	29	100.0	92	1 B69041	ribosomal protein
13	29	100.0	94	1 B64331	ribosomal protein
14	29	100.0	94	1 F75022	ribosomal protein
15	29	100.0	95	1 A90257	ribosomal protein
16	29	100.0	99	2 T08060	ribosomal protein
17	29	100.0	99	2 D97652	hypothetical prote
18	29	100.0	101	2 S04634	dipterocin D precu
19	29	100.0	101	2 C72467	hypothetical prote
20	29	100.0	102	2 JC1150	hypothetical prote
21	29	100.0	102	2 S21857	hypothetical prote
22	29	100.0	105	2 JC4923	ribosomal protein
23	29	100.0	105	2 A71405	ribosomal protein
24	29	100.0	106	1 R6HU36	ribosomal protein
25	29	100.0	106	1 R6RT36	ribosomal protein
26	29	100.0	106	1 R6UT6A	ribosomal protein
27	29	100.0	106	2 S32481	ribosomal protein
28	29	100.0	106	2 A43301	ribosomal protein
29	29	100.0	106	2 D43301	ribosomal protein

30	29	100.0	107	2 A70943	probable repressor
31	29	100.0	109	1 D71209	ribosomal protein
32	29	100.0	109	2 T40741	very hypothetical
33	29	100.0	112	2 H71041	hypothetical prote
34	29	100.0	120	2 E95343	hypothetical prote
35	29	100.0	121	2 S26798	ig heavy chain V r
36	29	100.0	125	2 S68170	ig heavy chain V r
37	29	100.0	125	2 B72517	hypothetical prote
38	29	100.0	128	2 G75308	hypothetical prote
39	29	100.0	129	1 A54119	c-type natriuratic
40	29	100.0	129	2 A85686	ribosomal holin pro
41	29	100.0	132	2 C70161	probable transcrip
42	29	100.0	132	2 H83048	hypothetical prote
43	29	100.0	133	2 S69322	hypothetical prote
44	29	100.0	137	2 I80176	class I histocompa
45	29	100.0	137	2 I38875	MHC class I antige

ALIGNMENTS

RESULT 1

F82394

hypothetical protein VCA0967 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: F82394

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
L, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: F82394

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-34 <HEI>

A;Cross-references: UNIPROT:Q9KKY3; GB:AE004423; GB:AE003853; NID:g9658400; PIDN:AAF9686

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VCA0967

A;Map position: 2

Query Match 100.0%; Score 29; DB 2; Length 34;

Best Local Similarity 40.0%; Pred. No. 84;

Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXXXXXGY 10

Db 21 RMNGRDCHGY 30

RESULT 2

S34045

protamine - North American opossum

C;Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossum)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: S34045

R;Winkfein, R.J.; Nishikawa, S.; Connor, W.; Dixon, G.H.

Eur J. Biochem. 215, 63-72, 1993

A;Title: Characterization of a marsupial sperm protamine gene and its transcripts from t

A;Reference number: S34045; MUID:93345500; PMID:8344286

A;Accession: S34045

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-58 <WIN>

A;Cross-references: UNIPROT:P35305; EMBL:X74044; NID:g407062; PIDN:CAA52193.1; PID:g4070

C;Superfamily: sperm histone

C;Keywords: DNA binding; nucleus

Query Match 100.0%; Score 29; DB 2; Length 58;

Best Local Similarity 40.0%; Pred. No. 1.4e+02;

Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 RXXRXRXGXG 10
      ||:::||
Db      35 RRRGRGRGY 44

RESULT 3
E90041
hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: E90041
R:Kuroda, M.; Ohca, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogino, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: E90041
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-60 <KUR>
A:Cross-references: UNIPROT:Q99RM5; GB:BA000018; PID:gl3702353; PIDN:BA43494.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA2192

      Query Match      100.0%; Score 29; DB 2; Length 60;
      Best Local Similarity 40.0%; Pred. No. 1.4e+02;
      Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 RXXRXRXGXG 10
      ||:::||
Db      34 RFILRTAIGY 43

RESULT 4
SBHUP
statherin precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: JH0153; A27308; B27489; A03288; A32524
R:Sabatini, L.M.; He, Y.Z.; Azen, E.A.
Gene 89, 245-251, 1990
A:Title: Structure and sequence determination of the gene encoding human salivary statherin
A:Reference number: JH0153; MUID:90323623; PMID:2373369
A:Accession: JH0153
A:Molecule type: DNA
A:Residues: 1-62 <SA2>
R:Sabatini, L.M.; Carlock, L.R.; Johnson, G.W.; Azen, E.A.
Am. J. Hum. Genet. 41, 1048-1060, 1987
A:Title: cDNA cloning and chromosomal localization (4q11-13) of a gene for statherin, a
A:Reference number: A27308; MUID:98074310; PMID:3502720
A:Accession: A27308
A:Molecule type: mRNA
A:Residues: 1-62 <SAB>
A:Cross-references: GB:M32639; NID:g338504; PIDN:AAA60593.1; PID:g338506
R:Dickinson, D.P.; Ridall, A.L.; Levine, M.J.
Biochem. Biophys. Res. Commun. 149, 784-790, 1987
A:Title: Human submandibular gland statherin and basic histidine-rich peptide are encoded
A:Reference number: A27489; MUID:88106506; PMID:3426601
A:Accession: B27489
A:Molecule type: mRNA
A:Residues: 1-62 <DIC>
A:Cross-references: GB:M18371; NID:g338610; PIDN:AAA60600.1; PID:g338611
R:Schlesinger, D.H.; Hay, D.I.
J. Biol. Chem. 252, 1689-1695, 1977
A:Title: Complete covalent structure of statherin, a tyrosine-rich acidic peptide which
A:Reference number: A03288; MUID:77118656; PMID:838735
A:Accession: A03288
A:Molecule type: protein
A:Residues: 20-62 <SCH>
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R:Oppenheim, F.G.; Hay, D.I.; Smith, D.J.; Offner, G.D.; Troxler, R.F.
J. Dent. Res. 66, 462-466, 1987
A:Title: Molecular basis of salivary proline-rich protein and peptide synthesis: cell-free
      gnal peptides.
A:Reference number: A92773; MUID:87309161; PMID:3476566
A:Accession: A32524
A:Molecule type: protein
A:Residues: 1,'X',3-4,'X',6,'X',8,'X',10,'X',12-13,'XX',16 <OPP>
A>Note: radiosequencing of precursor after cell-free translation
C:Comment: Statherin is one of the salivary proteins that stabilize saliva supersaturated
      bly being precursors of enamel pellicle). These inhibitors thus promote enamel stabilizat
C:Genetics:
A:Gene: GDS:STATH
A:Cross-references: GDS:120391; OMIM:184470
A:Map position: 4q11-4q13
A:Introns: 17/3; 24/3; 34/3
C:Superfamily: statherin precursor
C:Keywords: phosphoprotein; saliva
F:1-25/Domain: statherin/histatin signal sequence homology <SHH>
F:1-19/Domain: signal sequence #status experimental <SIG>
F:20-62/Product: statherin #status experimental <MAT>
F:21-22/Binding site: phosphate (Ser) (covalent) #status experimental

      Query Match      100.0%; Score 29; DB 1; Length 62;
      Best Local Similarity 40.0%; Pred. No. 1.5e+02;
      Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 RXXRXRXGXG 10
      ||:::||
Db      28 RRIGRPGYGY 37

RESULT 5
H72737
probable ribosomal protein L44 APES016 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: H72737
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaha
      awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ki
      DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: H72737
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-63 <KAW>
A:Cross-references: UNIPROT:Q9YF00; DDBJ:AP000059; NID:95103911; PIDN:BA479396.1; PID:dl
C:Genetics:
A:Gene: APES016
C:Superfamily: rat ribosomal protein L36a

      Query Match      100.0%; Score 29; DB 2; Length 63;
      Best Local Similarity 40.0%; Pred. No. 1.5e+02;
      Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 RXXRXRXGXG 10
      ||:::||
Db      6 RRYRRKQEGY 15

RESULT 6
AG1232
transcription regulator homolog lmo1263 [imported] - Listeria monocytogenes (strain EGD-e
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AG1232
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
      D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
      D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunat, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
```

ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria species*.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1232
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-71 <GLA>
A;Cross-references: UNIPROT:Q8Y7L4; GB:NC_003210; PIDN:CAC99341.1; PID:G16410679; GSPDB: A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo1263

Query Match 100.0%; Score 29; DB 2; Length 71;
Best Local Similarity 40.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXRXXXGY 10
|:::|:::|
Db 31 RMGYRTSGY 40

RESULT 7
D69010
hypothetical protein MTH108 - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
A;Accession: D69010
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N. ki, S.; Church, G.M.; Daniele, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional genome sequence
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: D69010
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-77 <MTH>
A;Cross-references: UNIPROT:Q26211; GB:AE000801; GB:AE000666; NID:G2621145; PIDN:AAH8461
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH108
A;Start codon: TTG

Query Match 100.0%; Score 29; DB 2; Length 77;
Best Local Similarity 40.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXRXXXGY 10
|:::|:::|
Db 65 RASYRLRVGY 74

RESULT 8
S68955
polyphenolic adhesive protein 3B precursor - Mediterranean mussel
N;Alternate names: foot protein 3B
C;Species: Mytilus galloprovincialis (Mediterranean mussel)
C;Date: 23-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
A;Accession: S68955
R;Inoue, K.; Takeuchi, Y.; Miki, D.; Odo, S.; Harayama, S.; Waite, J.H.
Eur. J. Biochem. 239, 172-176, 1996
A;Title: Cloning, sequencing and sites of expression of genes for the hydroxyarginine-co
A;Reference number: S68954; MUID:96305382; PMID:8706704
A;Accession: S68955
A;Molecule type: mRNA
A;Residues: 1-77 <INO>
A;Cross-references: UNIPROT:Q9GXU7
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-77/Product: polyphenolic adhesive protein 3B #status predicted <MAT>
F;27, 28, 32, 41, 44, 47, 52, 55, 58, 75, 77/Modified site: 3', 4'-dihydroxyphenylalanine (Tyr) #st
F;36, 37, 46, 50, 51, 63, 66, 67, 72, 73/Modified site: 4-hydroxyarginine (Arg) #status predicted

Query Match 100.0%; Score 29; DB 2; Length 77;

Best Local Similarity 40.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXRXXXGY 10
|:::|:::|
Db 46 RYNGRRYGGY 55

RESULT 9
S00265
dipterocin A - nestling-sucking blowfly
C;Species: Protophormia terraenovae (nestling-sucking blowfly)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
A;Accession: S00265
R;Dimarcq, J.L.; Keppi, E.; Dunbar, B.; Lambert, J.; Reichhart, J.M.; Hoffmann, D.; Rank
Eur. J. Biochem. 171, 17-22, 1988
A;Title: Insect immunity. Purification and characterization of a family of novel inducib
ence of the predominant member, dipterocin A.
A;Reference number: S00265; MUID:88111665; PMID:3276515
A;Accession: S00265
A;Molecule type: protein
A;Residues: 1-82 <DIM>
A;Cross-references: UNIPROT:P10836
C;Keywords: antibacterial

Query Match 100.0%; Score 29; DB 2; Length 82;
Best Local Similarity 40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXRXXXGY 10
|:::|:::|
Db 69 RPYRIGAGY 78

RESULT 10
T36233
hypothetical protein SCE39.23 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36233
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21577
A;Accession: T36233
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-88 <OLI>
A;Cross-references: UNIPROT:Q9X8E5; EMBL:AL049573; PIDN:CAB40331.1; GSPDB:GN00070; SCOE
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOE39.23

Query Match 100.0%; Score 29; DB 2; Length 88;
Best Local Similarity 40.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXRXXXGY 10
|:::|:::|
Db 21 RVDTRGVSGY 30

RESULT 11
G64381
ribosomal protein L34 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
A;Accession: G64381
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii

A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: G64381
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-89 <BUL>
A;Cross-references: UNIPROT:P54053; GB:U67513; GB:L77117; NID:g1591365; PIDN:AAB98650.1;
C;Genetics:
A;Map position: FOR583166-583435
C;Superfamily: rat ribosomal protein L34

Query Match 100.0%; Score 29; DB 2; Length 89;
Best Local Similarity 40.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXXXXXXGY 10
|:::|:::|
Db 63 RRPFRPYGGY 72

RESULT 12
B69041
ribosomal protein L36a.eR [similarity] - Methanobacterium thermoautotrophicum (strain De
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: B69041
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: B69041
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-92 <MTH>
A;Cross-references: UNIPROT:O27365; GB:AE000895; GB:AE000666; NID:g2622403; PIDN:AAB8578
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1310
C;Superfamily: rat ribosomal protein L36a
C;Keywords: protein biosynthesis; ribosome

Query Match 100.0%; Score 29; DB 1; Length 92;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXXXXXXGY 10
|:::|:::|
Db 38 RQFRVVTAGY 47

RESULT 13
B64331
ribosomal protein L36a.eR [similarity] - Methanococcus jannaschii
N;Alternate names: ribosomal protein ML44
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: B64331
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
i Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: B64331
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-94 <BUL>
A;Cross-references: UNIPROT:P54027; GB:U67480; GB:L77117; NID:g2826265; PIDN:AAB98236.1;
C;Genetics:
A;Map position: FOR235632-235916
C;Superfamily: rat ribosomal protein L36a

C;Keywords: protein biosynthesis; ribosome

Query Match 100.0%; Score 29; DB 1; Length 94;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXXXXXXGY 10
|:::|:::|
Db 38 RQFRVVTAGY 47

RESULT 14
F75022
ribosomal protein L36a.eR [similarity] - Pyrococcus abyssi (strain Orsay)
N;Alternate names: ribosomal protein L44e PAB1221
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: F75022
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: F75022
A;Molecule type: DNA
A;Residues: 1-94 <RAW>
A;Cross-references: UNIPROT:Q9UX22; GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB5062
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB1221
C;Superfamily: rat ribosomal protein L36a
C;Keywords: protein biosynthesis; ribosome

Query Match 100.0%; Score 29; DB 1; Length 94;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXXXXXXGY 10
|:::|:::|
Db 38 RRPFRILKGY 47

RESULT 15
A90257
ribosomal protein L36a.eR [similarity] - Sulfolobus solfataricus
N;Alternate names: ribosomal protein L44E
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: A90257
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-y
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: A90257
A;Molecule type: DNA
A;Residues: 1-95 <KUR>
A;Cross-references: UNIPROT:Q97281; GB:AE006641; NID:g13814234; PIDN:AAK41312.1; GSPDB:B
C;Genetics:
A;Gene: rpl44E
C;Superfamily: rat ribosomal protein L36a
C;Keywords: protein biosynthesis; ribosome

Query Match 100.0%; Score 29; DB 1; Length 95;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXXXXXXGY 10
|:::|:::|
Db 38 RRYERKNICY 47

Search completed: February 1, 2005, 07:01:30

Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 1, 2005, 06:44:50 ; Search time 195 Seconds
(without alignments)
29.506 Million cell updates/sec

Title: US-10-780-321-13
Perfect score: 29
Sequence: 1 RXXRXXXXGY 10

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02.*

- 1: uniprot_sprot.*
- 2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	34	2 Q9KKY3	Q9KKY3 vibrio chol
2	29	100.0	39	2 Q9XRV3	Q9XRV3 raistonia s
3	29	100.0	43	2 Q9KEJ5	Q9KEJ5 chlorobium
4	29	100.0	45	2 O18609	O18609 branchiosto
5	29	100.0	48	2 Q9TQC2	Q9TQC2 homo sapien
6	29	100.0	48	2 Q9TQC5	Q9TQC5 homo sapien
7	29	100.0	57	1 HSP1_DIDWA	P35305 didelphis m
8	29	100.0	60	1 HSP1_AEPRU	Q9G1P9 aepyprymus
9	29	100.0	60	2 Q6G6R7	Q6G6R7 staphylococ
10	29	100.0	60	2 Q6GE29	Q6GE29 staphylococ
11	29	100.0	60	2 Q9NV18	Q9NV18 staphylococ
12	29	100.0	60	2 Q9RMS5	Q9RMS5 staphylococ
13	29	100.0	60	2 Q7A3T4	Q7A3T4 staphylococ
14	29	100.0	60	2 Q9PYU9	Q9PYU9 xestia c-ni
15	29	100.0	61	1 HSP1_TRIVU	P42152 trichosurus
16	29	100.0	62	1 HSP1_SMIGR	Q9TUC3 sminthopsis
17	29	100.0	62	1 STAT_HUMAN	P02808 homo sapien
18	29	100.0	62	2 Q9CJCI	Q9CJCI rattus norv
19	29	100.0	62	2 AAH67219	AAH67219 homo sapi
20	29	100.0	63	1 HSP1_HYPMS	Q9GLQ1 hypsiprymo
21	29	100.0	63	1 RL44_AERPE	Q9YF00 aeropyrum p
22	29	100.0	63	2 Q6J1N4	Q6J1N4 burkholderi
23	29	100.0	63	2 Q6Z2B1	Q6Z2B1 oryza sativ
24	29	100.0	63	2 BAD01302	BAD01302 oryza sat
25	29	100.0	63	2 BAD01378	BAD01378 oryza sat
26	29	100.0	63	2 AAT38402	AAT38402 burkholde
27	29	100.0	65	2 Q9MHG7	Q9MHG7 pongo pygma
28	29	100.0	65	2 Q9MHG6	Q9MHG6 pongo pygma
29	29	100.0	65	2 Q7UX11	Q7UX11 rhodospirall
30	29	100.0	69	2 Q72BC9	Q72BC9 desulfobibr
31	29	100.0	69	2 AAS96184	AAS96184 desulfovib

32	29	100.0	71	2 Q6TLV6	Q6TLV6 macaca fasc
33	29	100.0	71	2 Q8GWM1	Q8GWM1 arabisdopsis
34	29	100.0	71	2 Q8Y7L4	Q8Y7L4 listeria mo
35	29	100.0	71	2 Q720F9	Q720F9 listeria mo
36	29	100.0	71	2 AAQ95597	AAQ95597 macaca fa
37	29	100.0	71	2 AAT04055	AAT04055 listeria
38	29	100.0	73	2 Q6K3X4	Q6K3X4 oryza sativ
39	29	100.0	74	2 Q86W88	Q86W88 homo sapien
40	29	100.0	74	2 Q99M07	Q99M07 mus musculu
41	29	100.0	75	2 Q9J870	Q9J870 spodoptera
42	29	100.0	76	2 Q30203	Q30203 homo sapien
43	29	100.0	76	2 Q8GI72	Q8GI72 salmonella
44	29	100.0	77	2 Q26211	Q26211 methanobact
45	29	100.0	77	2 Q9GUX7	Q9GUX7 mytilus gal

ALIGNMENTS

RESULT 1

ID	Q9KKY3	PRELIMINARY;	PRT;	34 AA.
AC	Q9KKY3;			
DT	01-OCT-2000 (TrEMBLrel. 15, Created)			
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	Hypothetical protein VCA0967.			
GN	OrderedLocusNames=VCA0967;			
OS	Vibrio cholerae.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;			
OC	Vibrionaceae; Vibrio.			
OX	NCBI_TaxID=666;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=El Tor N16961 / Serotype O1;			
RX	MEDLINE=20406833; Pubmed=10952301; DOI=10.1038/35020000;			
RA	Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,			
RA	Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,			
RA	Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,			
RA	Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,			
RA	Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,			
RA	Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,			
RA	Mekalanos J.J., Venter J.C., Fraser C.M.;			
RT	"DNA sequence of both chromosomes of the cholera pathogen Vibrio			
RT	cholerae."			
RL	Nature 406:477-483(2000).			
DR	EMBL; AE004423; AAF96863.1; -.			
DR	PIR; F82394; F82394.			
DR	TIGR; VCA0967; -.			
KW	Complete proteome; Hypothetical protein.			
SQ	SEQUENCE 34 AA; 3763 MW; 5CC9711DE0858E56 CRC64;			

Query Match 100.0%; Score 29; DB 2; Length 34;

Best Local Similarity 40.0%; Pred. No. 3.8e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 6;

Qy 1 RXXRXXXXGY 10

Db 21 RMNGRDCHGY 30

RESULT 2

ID	Q9XRV3	PRELIMINARY;	PRT;	39 AA.
AC	Q9XRV3;			
DT	01-MAR-2002 (TrEMBLrel. 20, Created)			
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	Hypothetical protein RSP0728.			
GN	Name=RS01700; OrderedLocusNames=RS0728;			
OS	Raistonia solanacearum (Pseudomonas solanacearum).			
OC	Plasmid megaplasmid.			
OC	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;			

```

OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Catolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siquier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646080; CAD17879.1; -.
KW Complete proteome; Hypothetical protein; Plasmid.
SQ SEQUENCE 39 AA; 4660 MW; EE5E40DA97913E5E CRC64;

Query Match 100.0%; Score 29; DB 2; Length 39;
Best Local Similarity 40.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXRXXXY 10
Db 24 RQYRRVTGV 33

RESULT 3
Q8KEJ5
ID Q8KEJ5 PRELIMINARY; PRT; 43 AA.
AC Q8KEJ5;
RX STRAIN=TL5 / ATCC 49652 / DSM 12025;
RC MEDLINE=22103685; PubMed=12093901; DOI=10.1073/pnas.132181499;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson B.J., DeBoy R.T., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.F., Yang F.,
RA Holt I.E., Umayam L.A., Mason T.M., Brenner M., Shea T.P.,
RA Parksey D.S., Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B.,
RA Radune D., Vamathevan J.J., Khouri H.M., White O., Gruber T.M.,
RA Ketchum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
DR EMBL; AE012841; AAM71931.1; -.
DR TIGR; CT0693; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 43 AA; 5354 MW; EFA76D438C1C2B7 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 43;
Best Local Similarity 40.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXRXXXY 10
Db 4 RYFIRLNGY 13

RESULT 4
O18609
ID O18609 PRELIMINARY; PRT; 45 AA.
AC O18609;
RX STRAIN=TL5 / ATCC 49652 / DSM 12025;
RC MEDLINE=22103685; PubMed=12093901; DOI=10.1073/pnas.132181499;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson B.J., DeBoy R.T., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.F., Yang F.,
RA Holt I.E., Umayam L.A., Mason T.M., Brenner M., Shea T.P.,
RA Parksey D.S., Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B.,
RA Radune D., Vamathevan J.J., Khouri H.M., White O., Gruber T.M.,
RA Ketchum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
DR EMBL; AE012841; AAM71931.1; -.
DR TIGR; CT0693; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 43 AA; 5354 MW; EFA76D438C1C2B7 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 48;
Best Local Similarity 40.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXRXXXY 10
Db 33 RESLRNLRGY 42

RESULT 5
Q9TQC2
ID Q9TQC2 PRELIMINARY; PRT; 48 AA.
AC Q9TQC2;
RX STRAIN=TL5 / ATCC 49652 / DSM 12025;
RC MEDLINE=22103685; PubMed=12093901; DOI=10.1073/pnas.132181499;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson B.J., DeBoy R.T., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.F., Yang F.,
RA Holt I.E., Umayam L.A., Mason T.M., Brenner M., Shea T.P.,
RA Parksey D.S., Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B.,
RA Radune D., Vamathevan J.J., Khouri H.M., White O., Gruber T.M.,
RA Ketchum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
DR EMBL; AE012841; AAM71931.1; -.
DR TIGR; CT0693; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 48 AA; 5841 MW; DFE6F652D5B60C3 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 48;
Best Local Similarity 40.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXRXXXY 10
Db 33 RESLRNLRGY 42

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DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DR Tr2 (Fragment).
OS Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7740;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97338099; PubMed=9192646;
RA Sacriava H., Safi R., Hanni C., Langlois M.C., Saumitou-Laprade P.,
RA Stehelin D., Capron A., Pierce R., Laudet V.;
RT "Ligand binding was acquired during evolution of nuclear receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:6803-6808(1997).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR EMBL; U93412; AAB68692.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00105; zf-C4; 1.
DR SMART; SM00399; Znf_C4; 1.
KW DNA-binding; Metal-Binding; Nuclear protein; Receptor;
KW Transcription regulation; Zinc; Zinc-finger.
FT NON_TER 1
FT NON_TER 45
SQ SEQUENCE 45 AA; 5415 MW; F509F0B07377F793 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 45;
Best Local Similarity 40.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXRXXXY 10
Db 6 RRSIRKNGY 15

RESULT 5
Q9TQC2
ID Q9TQC2 PRELIMINARY; PRT; 48 AA.
AC Q9TQC2;
RX STRAIN=TL5 / ATCC 49652 / DSM 12025;
RC MEDLINE=22103685; PubMed=12093901; DOI=10.1073/pnas.132181499;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson B.J., DeBoy R.T., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.F., Yang F.,
RA Holt I.E., Umayam L.A., Mason T.M., Brenner M., Shea T.P.,
RA Parksey D.S., Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B.,
RA Radune D., Vamathevan J.J., Khouri H.M., White O., Gruber T.M.,
RA Ketchum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
DR EMBL; AE012841; AAM71931.1; -.
DR TIGR; CT0693; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 43 AA; 5354 MW; EFA76D438C1C2B7 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 43;
Best Local Similarity 40.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXRXXXY 10
Db 4 RYFIRLNGY 13

RESULT 4
O18609
ID O18609 PRELIMINARY; PRT; 45 AA.
AC O18609;
RX STRAIN=TL5 / ATCC 49652 / DSM 12025;
RC MEDLINE=22103685; PubMed=12093901; DOI=10.1073/pnas.132181499;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson B.J., DeBoy R.T., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.F., Yang F.,
RA Holt I.E., Umayam L.A., Mason T.M., Brenner M., Shea T.P.,
RA Parksey D.S., Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B.,
RA Radune D., Vamathevan J.J., Khouri H.M., White O., Gruber T.M.,
RA Ketchum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
DR EMBL; AE012841; AAM71931.1; -.
DR TIGR; CT0693; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 43 AA; 5354 MW; EFA76D438C1C2B7 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 48;
Best Local Similarity 40.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXRXXXY 10
Db 33 RESLRNLRGY 42

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DR EMBL; L17007; AAA02812.1; -
DR EMBL; X74044; CAA52193.1; -
DR EMBL; L35448; AAA74612.1; -
DR PIR; S34045; S34045
DR InterPro; IPR000221; Protamine_P1.
DR Pfam; PF00260; Protamine_P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
DR Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
KW Nucleosome core; Spermatogenesis; Testis.
FT INIT MET 0 0 By similarity.
SQ SEQUENCE 57 AA; 7810 MW; 283715B280214E52 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 57;
Best Local Similarity 40.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXRXXXXGY 10
Db 34 RRRGRGRGY 43

RESULT 8
HSPI_AEPFU STANDARD; PRT; 60 AA.
AC Q9GLF9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sperm protamine P1.
GN Names=PRMI;
OS Aepyrymnus rufescens (Rufous rat-kangaroo) (Rufous bettong).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Potoroidae; Aepyrymnus.
OX NCBI_TaxID=38598;
RN [1]
RP SEQUENCE FROM N.A.
RA Burk A., Springer M.S.;
RT "Intergenic relationships among Macropodoidea (Metatheria:
RL J. Mammal. Evol. 7:213-237(2000).
CC -1- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Testis.
CC -1- SIMILARITY: Belongs to the protamine P1 family.
CC -----
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CC -----
DR EMBL; AF187547; AAC27964.1; -
DR InterPro; IPR000221; Protamine_P1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
KW Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
KW Nucleosome core; Spermatogenesis; Testis.
FT INIT MET 0 0 By similarity.
SQ SEQUENCE 60 AA; 8445 MW; 1DC24691644A17E0 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 60;
Best Local Similarity 40.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXRXXXXGY 10
Db 33 RRRGRGRGY 42

RESULT 7
HSPI_DIDMA STANDARD; PRT; 57 AA.
ID HSPI_DIDMA STANDARD; PRT; 57 AA.
AC P35305;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sperm protamine P1.
GN Names=PRMI;
OS Didelphis marsupialis virginiana (North American opossum), and
OS Monodelphis domestica (Short-tailed grey opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9267, 13616;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=D.marsupialis;
RX MEDLINE=9345500; PubMed=8344286;
RA Winkfein R.J., Nishikawa S., Connor W., Dixon G.H.;
RT "Characterization of a marsupial sperm protamine gene and its
RL transcripts from the North American opossum (Didelphis marsupialis).";
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.domestica;
RX MEDLINE=95215351; PubMed=7700877;
RA Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
RT "Molecular phylogeny and evolution of marsupial protamine P1 genes.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
CC -1- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Testis.
CC -1- SIMILARITY: Belongs to the protamine P1 family.
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CC -----
DR EMBL; L17007; AAA02812.1; -
DR EMBL; X74044; CAA52193.1; -
DR EMBL; L35448; AAA74612.1; -
DR PIR; S34045; S34045
DR InterPro; IPR000221; Protamine_P1.
DR Pfam; PF00260; Protamine_P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
DR Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
KW Nucleosome core; Spermatogenesis; Testis.
FT INIT MET 0 0 By similarity.
SQ SEQUENCE 57 AA; 7810 MW; 283715B280214E52 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 57;
Best Local Similarity 40.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXRXXXXGY 10
Db 34 RRRGRGRGY 43

RESULT 8
HSPI_AEPFU STANDARD; PRT; 60 AA.
AC Q9GLF9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sperm protamine P1.
GN Names=PRMI;
OS Aepyrymnus rufescens (Rufous rat-kangaroo) (Rufous bettong).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Potoroidae; Aepyrymnus.
OX NCBI_TaxID=38598;
RN [1]
RP SEQUENCE FROM N.A.
RA Burk A., Springer M.S.;
RT "Intergenic relationships among Macropodoidea (Metatheria:
RL J. Mammal. Evol. 7:213-237(2000).
CC -1- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Testis.
CC -1- SIMILARITY: Belongs to the protamine P1 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF187547; AAC27964.1; -
DR InterPro; IPR000221; Protamine_P1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
KW Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
KW Nucleosome core; Spermatogenesis; Testis.
FT INIT MET 0 0 By similarity.
SQ SEQUENCE 60 AA; 8445 MW; 1DC24691644A17E0 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 60;
Best Local Similarity 40.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXRXXXXGY 10
Db 33 RRRGRGRGY 42

RESULT 7
HSPI_DIDMA STANDARD; PRT; 57 AA.
ID HSPI_DIDMA STANDARD; PRT; 57 AA.
AC P35305;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sperm protamine P1.
GN Names=PRMI;
OS Didelphis marsupialis virginiana (North American opossum), and
OS Monodelphis domestica (Short-tailed grey opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9267, 13616;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=D.marsupialis;
RX MEDLINE=9345500; PubMed=8344286;
RA Winkfein R.J., Nishikawa S., Connor W., Dixon G.H.;
RT "Characterization of a marsupial sperm protamine gene and its
RL transcripts from the North American opossum (Didelphis marsupialis).";
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.domestica;
RX MEDLINE=95215351; PubMed=7700877;
RA Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
RT "Molecular phylogeny and evolution of marsupial protamine P1 genes.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
CC -1- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Testis.
CC -1- SIMILARITY: Belongs to the protamine P1 family.
-----
```

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Best Local Similarity 40.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXXRXXXXGY 10
Db 39 RSRRRRRRGY 48

RESULT 9
Q6G6R7
ID Q6G6R7 PRELIMINARY; PRT; 60 AA.
AC Q6G6R7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative membrane protein.
GN ORFNames=SAS2295;
OS Staphylococcus aureus subsp. aureus MSSA476.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]_SEQUENCE FROM N.A.
RC STRAIN=MSSA476;
RA Holden M.T.G., Feil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571857; CAG44108.1; -.
SQ SEQUENCE 60 AA; 6962 MW; F0136267172B5B22 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 60;
Best Local Similarity 40.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXXRXXXXGY 10
Db 34 RLRLTAIGY 43

RESULT 10
Q6GE29
ID Q6GE29 PRELIMINARY; PRT; 60 AA.
AC Q6GE29;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative membrane protein.
GN ORFNames=SAR2494;
OS Staphylococcus aureus subsp. aureus MRSA252.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]_SEQUENCE FROM N.A.
RC STRAIN=MRSA252;
RA Holden M.T.G., Feil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
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RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571856; CAG41474.1; -.
SQ SEQUENCE 60 AA; 6931 MW; 6D66A17886A0186B CRC64;

Query Match 100.0%; Score 29; DB 2; Length 60;
Best Local Similarity 40.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXXRXXXXGY 10
Db 34 RFLRLTVGY 43

RESULT 11
Q8NV18
ID Q8NV18 PRELIMINARY; PRT; 60 AA.
AC Q8NV18;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein MW2326.
GN OrderedLocusNames=MW2326;
OS Staphylococcus aureus (Strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]_SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwana N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL; AP04830; BAB96191.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 60 AA; 6962 MW; F0136267172B5B22 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 60;
Best Local Similarity 40.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXXRXXXXGY 10
Db 34 RFLRLTAIGY 43

RESULT 12
Q99RM5
ID Q99RM5 PRELIMINARY; PRT; 60 AA.
AC Q99RM5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=SAV2404;
OS Staphylococcus aureus (Strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]_SEQUENCE FROM N.A.
RC STRAIN=MU50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohca T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
```

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RL Lancet 357:1225-1240(2001).
DR EMBL: AP003365; BAB58566.1; -.
DR PIR: E90041; E90041.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 60 AA; 6976 MW; 1CC36267172B5B3A CRC64;

Query Match 100.0%; Score 29; DB 2; Length 60;
Best Local Similarity 40.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXRXXXXY 10
Db 34 RFLRTAIGY 43

RESULT 13
Q7A3T4 PRELIMINARY; PRT; 60 AA.
ID O7A3T4
AC O7A3T4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein SA2192.
GN OrderedLocusNames=SA2192;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yanashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogaewara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL: AP003137; BAB43494.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 60 AA; 6976 MW; 1CC36267172B5B3A CRC64;

Query Match 100.0%; Score 29; DB 2; Length 60;
Best Local Similarity 40.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXRXXXXY 10
Db 34 RFLRTAIGY 43

RESULT 14
Q9PYU9 PRELIMINARY; PRT; 60 AA.
ID Q9PYU9
AC Q9PYU9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ORF94.
GN Name=ORF94;
OS Xestia c-nigrum granulosis virus (XnGV) (Xestia c-nigrum
OS Granulovirus).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
OX NCBI_TaxID=51677;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99434230; PubMed=10502508;
RA Hayakawa T., Ko R., Okano K., Seong S.-I., Goto C., Maeda S.;
RT "Sequence analysis of the Xestia c-nigrum granulovirus genome.";
RL Virology 262:277-297(1999).
DR EMBL: AF162221; AAF05208.1; -.

SQ SEQUENCE 60 AA; 7452 MW; B477BAF7DB2D5930 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 60;
Best Local Similarity 40.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXRXXXXY 10
Db 34 RRRSRRSRGY 43

RESULT 15
HSPI_TRIUV STANDARD; PRT; 61 AA.
ID HSPI_TRIUV
AC P42152;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sperm protamine P1.
GN Name=PRMI;
OS Trichosurus vulpecula (Brush-tailed possum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
OX NCBI_TaxID=9337;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Sperm;
RX MEDLINE=95215351; PubMed=7700877;
RA Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
RT "Molecular phylogeny and evolution of marsupial protamine P1 genes.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
CC -1- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Testis.
CC -1- SIMILARITY: Belongs to the protamine P1 family.
CC
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CC
CC EMBL: L32744; AAA99479.1; -.
CC InterPro: IPR000221; Protamine_P1.
CC Pfam: PF00260; Protamine_P1; 1.
CC PROSITE: PS00048; PROTAMINE_P1; 1.
CC Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
CC Nucleosome core; Spermatogenesis; Testis.
CC INIT MET 0 0 By similarity.
CC SEQUENCE 61 AA; 8571 MW; 802287E627EE816C CRC64;

Query Match 100.0%; Score 29; DB 1; Length 61;
Best Local Similarity 40.0%; Pred. No. 7e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXRXXXXY 10
Db 39 RRRRRRRRGY 48

Search completed: February 1, 2005, 07:00:46
Job time : 198 secs
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OM protein - protein search, using sw model

Run on: February 1, 2005, 06:44:50 ; Search time 66 Seconds
(without alignments)
54.353 Million cell updates/sec

Title: US-10-780-321-13

Perfect score: 29

Sequence: 1 RXXRXRXGXG 10

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext. 0.5

Searched: 200273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 200273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	10	2 AAR41209	Aar41209 Peptide f
2	29	100.0	10	2 AAR83061	Aar83061 HLA-B7 CT
3	29	100.0	10	2 AAW07518	Aaw07518 T-cell mo
4	29	100.0	10	2 AAW07517	Aaw07517 T-cell mo
5	29	100.0	10	2 AAW07515	Aaw07515 T-cell mo
6	29	100.0	10	2 AAW82806	Aaw82806 Cytomodul
7	29	100.0	10	2 AAW82819	Aaw82819 Cytomodul
8	29	100.0	10	2 AAW82807	Aaw82807 Cytomodul
9	29	100.0	10	2 AAW82809	Aaw82809 Cytomodul
10	29	100.0	10	2 AAW82822	Aaw82822 Cytomodul
11	29	100.0	10	2 AAW82811	Aaw82811 Cytomodul
12	29	100.0	10	2 AAW82816	Aaw82816 Cytomodul
13	29	100.0	10	2 AAW82820	Aaw82820 Cytomodul
14	29	100.0	10	2 AAW82827	Aaw82827 Cytomodul
15	29	100.0	10	2 AAW82821	Aaw82821 Cytomodul
16	29	100.0	10	2 AAW82824	Aaw82824 Cytomodul
17	29	100.0	10	2 AAW82828	Aaw82828 Cytomodul
18	29	100.0	10	2 AAW82804	Aaw82804 Cytomodul
19	29	100.0	10	2 AAW82817	Aaw82817 Cytomodul
20	29	100.0	10	2 AAW82826	Aaw82826 Cytomodul
21	29	100.0	10	2 AAW82829	Aaw82829 Cytomodul
22	29	100.0	10	2 AAW82810	Aaw82810 Cytomodul
23	29	100.0	10	2 AAW82805	Aaw82805 Cytomodul
24	29	100.0	10	2 AAW82813	Aaw82813 Cytomodul
25	29	100.0	10	2 AAW82823	Aaw82823 Cytomodul

26	29	100.0	10	2 AAW82808	Aaw82808 Cytomodul
27	29	100.0	10	2 AAW82814	Aaw82814 Cytomodul
28	29	100.0	10	2 AAW82818	Aaw82818 Cytomodul
29	29	100.0	10	2 AAW82812	Aaw82812 Cytomodul
30	29	100.0	10	2 AAW82815	Aaw82815 Cytomodul
31	29	100.0	10	2 AAW82825	Aaw82825 Cytomodul
32	29	100.0	10	2 AAW33796	Aaw33796 Peptide B
33	29	100.0	10	2 AAW33786	Aaw33786 Peptide B
34	29	100.0	10	4 AAY72486	Aay72486 Immunoeup
35	29	100.0	10	4 AAY72485	Aay72485 Immunoeup
36	29	100.0	10	4 AAY72496	Aay72496 Immunoeup
37	29	100.0	10	4 AAY72494	Aay72494 Immunoeup
38	29	100.0	10	4 AAY72487	Aay72487 Immunoeup
39	29	100.0	10	4 AAY72497	Aay72497 Immunoeup
40	29	100.0	10	4 AAY72495	Aay72495 Immunoeup
41	29	100.0	10	4 AAY72493	Aay72493 Immunoeup
42	29	100.0	10	6 ABR24478	Abr24478 Human can
43	29	100.0	10	6 ABR25732	Abr25732 Human can
44	29	100.0	10	6 ABR25113	Abr25113 Human can
45	29	100.0	10	6 ABR24876	Abr24876 Human can

ALIGNMENTS

RESULT 1

AAR41209
ID AAR41209 standard; peptide; 10 AA.

XX AAR41209;

XX 25-MAR-2003 (revised)

DT 15-MAR-1994 (first entry)

XX XX

DE Peptide fragment of Class I HLA peptide.

XX Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
KW parasitic disease; cytotoxic T lymphocyte; modulation.
XX Synthetic.

XX OS

XX WO9317699-A1.

PN 16-SEP-1993.

XX 25-FEB-1993; 93WO-US001758.

XX 02-MAR-1992; 92US-00844716.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Clayberger CA, Krensky AM;

XX WPI; 1993-303134/38.

XX New peptide(s) based on Class I HLA antigen domains - used for modulating
cycotoxic T-lymphocyte activity towards targets.
PS Claim 11; Page 54; 61pp; English.

XX The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity,
either by inhibition or stimulation. It can be used for inhibiting CTL
toxicity in transplantations, for inducing CTL activity in parasitic
diseases and neoplasia and in studies on viral infection. The peptide can
also be used for identifying CTLs which bind to it and removing subsets
of CTLs from a T-cell composition. This peptide sequence is more commonly
found within larger peptide compounds of not more than 30 amino acids in
length. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 10 AA;

Query Match 100.0%; Score 29; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 2.2e+02;

```

Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXXRXXGXG 10
   |::|::|
Db 1 RSLRLRGY 10

RESULT 2
AAR83061
ID AAR83061 standard; peptide; 10 AA.
XX
AC AAR83061;
XX
DT 15-MAY-1996 (first entry)
XX
DE HLA-B7 CTL modulating peptide (B7.75-84).
XX
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B7.
XX
OS Synthetic.
XX
PN WO9526979-A1.
XX
PD 12-OCT-1995.
XX
PF 05-APR-1995; 95WO-US004349.
XX
PR 05-APR-1994; 94US-00222851.
XX
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI Clayberger C, Krensky AM, Parham P;
XX
DR WPI; 1995-358582/46.
XX
PT Extension of acceptance period of transplants from MHC unmatched donor
PT hosts - using Class I B75-84 MHC antigen of the recipient host.
XX
PS Claim 13; Page 66; 80pp; English.
XX
SS This sequence represents a fragment of a class I major histocompatibility
CC complex (MHC) antigen. This sequence corresponds to residues 75-84 of the
CC alpha-1 domain of the class I MHC HLA-B7. This sequence, and the peptide
CC fragments represented by AAR83062-R83085, AAR83090-R83096 and AAR82807-
CC R92913 can be used to extend the period of acceptance by a recipient of a
CC transplant from an MHC unmatched donor. The peptides are administered to
CC a patient in conjunction with a subtherapeutic amount of an
CC immunosuppressant. This is administered to the patient for a limited
CC period of time (compared to the lifetime administration for current
CC treatments). The peptides particularly modulate (or inhibit) the activity
CC of the cytotoxic T lymphocytes (CTLs) of the patient
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 29; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXXRXXGXG 10
   |::|::|
Db 1 RSLRLRGY 10

RESULT 3
AAR83061
ID AAR83061 standard; peptide; 10 AA.
XX
AC AAR83061;
XX
DT 04-AUG-1997 (first entry)
XX

```

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DE XX T-cell modulating peptide #7.
KW T-cell modulator; autoimmune disease; tissue destruction; alaph-domain;
KW mammal; major histocompatibility complex; MHC class I; antigen; perforin;
KW insulin-dependent diabetes mellitus; multiple sclerosis; inflammation;
KW rheumatoid arthritis; psoriasis; pemphigus vulgaris; Sjogren's disease;
KW thyroid disease; Hashimoto's thyroiditis; myasthenia gravis; granzyme;
KW autologous target cell; cytokine release; T cell activation; therapy.
XX
OS Synthetic.
XX
PN WO9635443-A1.
XX
PD 14-NOV-1996.
XX
PF 05-APR-1996; 96WO-US004710.
XX
PR 12-MAY-1995; 95US-00440504.
XX
PA (SANG-) SANGSTAT MEDICAL CORP.
XX
PI Buelow R;
XX
DR WPI; 1996-518410/51.
XX
PT Treatment of auto-immune disease by admin. of peptide(s) corresp. to
PT major histocompatibility complex antigens - esp. for delaying onset of
PT clinical symptoms of insulin dependent diabetes by modulating T cell
PT mediated attack on target cells.
XX
PS Claim 7; Page 20; 24pp; English.
XX
CC AAW07512-W07518 represent T-cell modulating peptides that can be used in
CC the method of the invention. These sequences are based on a portion of
CC the generic peptide corresponding to residues 70-91 of the alaph-domain
CC of the major histocompatibility complex (MHC) class I antigen (see
CC AAW07510). The method is for affecting the course of an autoimmune
CC disease involving T-cell mediated destruction of tissue in mammals. These
CC peptides are used especially to treat insulin-dependent diabetes
CC mellitus, preferably being administered during the pre-clinical stage to
CC delay onset of the disease. Other diseases that can be treated are
CC multiple sclerosis, rheumatoid arthritis, psoriasis, pemphigus vulgaris,
CC Sjogren's disease, thyroid disease, Hashimoto's thyroiditis, myasthenia
CC gravis, etc. The peptides modulate T-cell mediated attack on autologous
CC target cells, and may also reduce inflammation, swelling, and release of
CC cytokines, perforins, granzymes etc. associated with T cell activation
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 29; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXXRXXGXG 10
   |::|::|
Db 1 RSLRLRGY 10

RESULT 4
AAR83061
ID AAR83061 standard; peptide; 10 AA.
XX
AC AAR83061;
XX
DT 04-AUG-1997 (first entry)
XX
DE T-cell modulating peptide #6.
XX
KW T-cell modulator; autoimmune disease; tissue destruction; alaph-domain;
KW mammal; major histocompatibility complex; MHC class I; antigen; perforin;
KW insulin-dependent diabetes mellitus; multiple sclerosis; inflammation;
KW rheumatoid arthritis; psoriasis; pemphigus vulgaris; Sjogren's disease;
KW thyroid disease; Hashimoto's thyroiditis; myasthenia gravis; granzyme;

```

KW autologous target cell; cytokine release; T cell activation; therapy.
 XX Synthetic.
 OS
 PN WO9635443-A1.
 XX
 XX
 PD 14-NOV-1996.
 XX
 XX
 PF 05-APR-1996; 96WO-US004710.
 XX
 PR 12-MAY-1995; 95US-00440504.
 XX
 PA (SANG-) SANGSTAT MEDICAL CORP.
 XX
 PI Buelow R;
 XX
 DR WPI; 1996-518410/51.
 XX
 PT Treatment of auto-immune disease by admin. of peptide(s) corresp. to
 PT major histocompatibility complex antigens - esp. for delaying onset of
 PT clinical symptoms of insulin dependent diabetes by modulating T cell
 PT mediated attack on target cells.
 XX
 PS Claim 7; Page 20; 24pp; English.
 XX
 CC AA07512-W07518 represent T-cell modulating peptides that can be used in
 CC the method of the invention. These sequences are based on a portion of
 CC the generic peptide corresponding to residues 70-91 of the alpha1-domain
 CC of the major histocompatibility complex (MHC) class I antigen (see
 CC AA07510). The method is for affecting the course of an autoimmune
 CC disease involving T-cell mediated destruction of tissue in mammals. These
 CC peptides are used especially to treat insulin-dependent diabetes
 CC mellitus, preferably being administered during the pre-clinical stage to
 CC delay onset of the disease. Other diseases that can be treated are
 CC multiple sclerosis, rheumatoid arthritis, psoriasis, pemphigus vulgaris,
 CC Sjogren's disease, thyroid disease, Hashimoto's thyroiditis, myasthenia
 CC gravis, etc. The peptides modulate T-cell mediated attack on autologous
 CC target cells, and may also reduce inflammation, swelling, and release of
 CC cytokines, perforins, granzymes etc. associated with T cell activation
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 29; DB 2; Length 10;
 Best Local Similarity 40.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RXXXXXXGY 10
 Db |:::|:::|
 1 RVDLTLLGY 10
 RESULT 5
 AA07515
 ID AA07515 standard; peptide; 10 AA.
 AC AA07515;
 XX
 DT 04-AUG-1997 (first entry)
 XX
 DE T-cell modulating peptide #4.
 XX
 KW T-cell modulator; autoimmune disease; tissue destruction; alpha1-domain;
 KW mammal; major histocompatibility complex; MHC class I; antigen; perforin;
 KW insulin-dependent diabetes mellitus; multiple sclerosis; inflammation;
 KW rheumatoid arthritis; psoriasis; pemphigus vulgaris; Sjogren's disease;
 KW thyroid disease; Hashimoto's thyroiditis; myasthenia gravis; granzyme;
 KW autologous target cell; cytokine release; T cell activation; therapy.
 XX
 OS Synthetic.
 XX
 PN WO9635443-A1.
 XX
 PD 14-NOV-1996.

XX
 PF 05-APR-1996; 96WO-US004710.
 XX
 PR 12-MAY-1995; 95US-00440504.
 XX
 PA (SANG-) SANGSTAT MEDICAL CORP.
 XX
 PI Buelow R;
 XX
 DR WPI; 1996-518410/51.
 XX
 PT Treatment of auto-immune disease by admin. of peptide(s) corresp. to
 PT major histocompatibility complex antigens - esp. for delaying onset of
 PT clinical symptoms of insulin dependent diabetes by modulating T cell
 PT mediated attack on target cells.
 XX
 PS Claim 7; Page 20; 24pp; English.
 XX
 CC AA07512-W07518 represent T-cell modulating peptides that can be used in
 CC the method of the invention. These sequences are based on a portion of
 CC the generic peptide corresponding to residues 70-91 of the alpha1-domain
 CC of the major histocompatibility complex (MHC) class I antigen (see
 CC AA07510). The method is for affecting the course of an autoimmune
 CC disease involving T-cell mediated destruction of tissue in mammals. These
 CC peptides are used especially to treat insulin-dependent diabetes
 CC mellitus, preferably being administered during the pre-clinical stage to
 CC delay onset of the disease. Other diseases that can be treated are
 CC multiple sclerosis, rheumatoid arthritis, psoriasis, pemphigus vulgaris,
 CC Sjogren's disease, thyroid disease, Hashimoto's thyroiditis, myasthenia
 CC gravis, etc. The peptides modulate T-cell mediated attack on autologous
 CC target cells, and may also reduce inflammation, swelling, and release of
 CC cytokines, perforins, granzymes etc. associated with T cell activation
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 29; DB 2; Length 10;
 Best Local Similarity 40.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RXXXXXXGY 10
 Db |:::|:::|
 1 RESLNRLGY 10
 RESULT 6
 AA07515
 ID AA07515 standard; peptide; 10 AA.
 AC AA07515;
 XX
 DT 28-JAN-1999 (first entry)
 XX
 DE Cytomodulating lipophilic oligopeptide (c).
 XX
 KW Cytomodulating lipophilic oligopeptide; immune system; inflammation;
 KW cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T cell;
 KW B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis;
 KW Crohn's disease; colitis; allergy; transplant.
 XX
 OS Synthetic.
 XX
 PN WO9846633-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 10-APR-1998; 98WO-US007231.
 XX
 PR 11-APR-1997; 97US-00838916.
 XX
 PR 23-FEB-1998; 98US-00028083.
 XX
 PA (SANG-) SANGSTAT MEDICAL CORP.
 XX
 PI Buelow R, Grassy G, Calas B;

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XX WPI; 1998-594558/50.
XX
XX New lipophilic peptide(s) that inhibit activation of immune system cells
PT - used for, e.g. production of cytokine(s) and the inflammatory response,
PT and also for modulating haem-containing enzymes.
XX
XX Claim 7; Page 37; 48pp; English.
XX
XX AAW82804 to AAW82829 are cytomodulating lipophilic oligopeptides. The
CC oligopeptides are used to inhibit: (i) activity of lymphocytes
CC (particularly cytotoxic T cells, but also natural killers, B cells and
CC mononuclear phagocytes); (ii) production of inflammatory cytokines, and
CC (iii) an inflammatory response in mammals (e.g. in cases of septic shock,
CC rheumatoid arthritis (RA), Crohn's disease, colitis and allergy). They
CC are also used for modulating activity of haem-containing enzymes and for
CC delaying onset of autoimmune disease (specifically insulin-dependent
CC diabetes mellitus, RA and systemic lupus erythematosus). In all cases the
CC oligopeptides may be generated from nucleic acids, and treatments are in
CC vitro or in vivo. A specific application is treatment of organs or cells
CC for transplantation, or of the recipient of such transplants. Apart from
CC therapeutic use, the oligopeptides can be used to study mechanisms of T
CC cell (de)activation and to raise antibodies (used to identify
CC of the oligopeptides). The oligopeptides are administered by bolus
CC injection or infusion, typically at 0.1-50 (preferably 1-25) mg/kg.
CC Treatment with the oligopeptides increases the life of transplants
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 29; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXXRXXXXGY 10
DB |:::|:::|
1 RLLRLLLGY 10

RESULT 7
AAW82819
ID AAW82819 standard; peptide; 10 AA.
XX
AC AAW82819;
XX
DT 28-JAN-1999 (first entry)
XX
DE Cytomodulating lipophilic oligopeptide (p).
XX
XX Cytomodulating lipophilic oligopeptide; immune system; inflammation;
KW cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T cell;
KW B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis;
KW Crohn's disease; colitis; allergy; transplant.
XX
OS Synthetic.
XX
PN WO9846633-A1.
XX
PD 22-OCT-1998.
XX
PF 10-APR-1998; 98WO-US007231.
XX
PR 11-APR-1997; 97US-00838916.
XX
PR 23-FEB-1998; 98US-00028083.
XX
PA (SANG-) SANGSTAT MEDICAL CORP.
XX
PI Buelow R, Grassy G, Calas B;
XX
PI WPI; 1998-594558/50.
XX
XX New lipophilic peptide(s) that inhibit activation of immune system cells
PT - used for, e.g. production of cytokine(s) and the inflammatory response,
PT and also for modulating haem-containing enzymes.
XX
XX Claim 7; Page 37; 48pp; English.
XX
XX AAW82804 to AAW82829 are cytomodulating lipophilic oligopeptides. The
CC oligopeptides are used to inhibit: (i) activity of lymphocytes
CC (particularly cytotoxic T cells, but also natural killers, B cells and
CC mononuclear phagocytes); (ii) production of inflammatory cytokines, and
CC (iii) an inflammatory response in mammals (e.g. in cases of septic shock,
CC rheumatoid arthritis (RA), Crohn's disease, colitis and allergy). They
CC are also used for modulating activity of haem-containing enzymes and for
CC delaying onset of autoimmune disease (specifically insulin-dependent
CC diabetes mellitus, RA and systemic lupus erythematosus). In all cases the
CC oligopeptides may be generated from nucleic acids, and treatments are in
CC vitro or in vivo. A specific application is treatment of organs or cells
CC for transplantation, or of the recipient of such transplants. Apart from
CC therapeutic use, the oligopeptides can be used to study mechanisms of T
CC cell (de)activation and to raise antibodies (used to identify
CC of the oligopeptides). The oligopeptides are administered by bolus
CC injection or infusion, typically at 0.1-50 (preferably 1-25) mg/kg.
CC Treatment with the oligopeptides increases the life of transplants
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 29; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXXRXXXXGY 10
DB |:::|:::|
1 RLLRLLLGY 10

RESULT 8
AAW82807
ID AAW82807 standard; peptide; 10 AA.
XX
AC AAW82807;
XX
DT 28-JAN-1999 (first entry)
XX
DE Cytomodulating lipophilic oligopeptide (d).
XX
XX Cytomodulating lipophilic oligopeptide; immune system; inflammation;
KW cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T cell;
KW B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis;
KW Crohn's disease; colitis; allergy; transplant.
XX
OS Synthetic.
XX
PN WO9846633-A1.
XX
PD 22-OCT-1998.
XX
PF 10-APR-1998; 98WO-US007231.
XX
PR 11-APR-1997; 97US-00838916.
XX
PR 23-FEB-1998; 98US-00028083.
XX
PA (SANG-) SANGSTAT MEDICAL CORP.
XX
PI Buelow R, Grassy G, Calas B;
XX
PI WPI; 1998-594558/50.
XX
XX New lipophilic peptide(s) that inhibit activation of immune system cells
PT - used for, e.g. production of cytokine(s) and the inflammatory response,
PT and also for modulating haem-containing enzymes.
XX
XX Claim 7; Page 37; 48pp; English.
XX
XX AAW82804 to AAW82829 are cytomodulating lipophilic oligopeptides. The

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CC oligopeptides are used to inhibit: (i) activity of lymphocytes
 CC (particularly cytotoxic T cells, but also natural killers, B cells and
 CC mononuclear phagocytes); (ii) production of inflammatory cytokines, and
 CC (iii) an inflammatory response in mammals (e.g. in cases of septic shock,
 CC rheumatoid arthritis (RA), Crohn's disease, colitis and allergy). They
 CC are also used for modulating activity of haem-containing enzymes and for
 CC delaying onset of autoimmune disease (specifically insulin-dependent
 CC diabetes mellitus, RA and systemic lupus erythematosus). In all cases the
 CC oligopeptides may be generated from nucleic acids, and treatments are in
 CC vitro or in vivo. A specific application is treatment of organs or cells
 CC for transplantation, or of the recipient of such transplants. Apart from
 CC therapeutic use, the oligopeptides can be used to study mechanisms of T
 CC cell (de)activation and to raise antibodies (used to identify
 CC oligopeptides and to raise anti-idiotypic antibodies that are competitors
 CC of the oligopeptides). The oligopeptides are administered by bolus
 CC injection or infusion, typically at 0.1-50 (preferably 1-25) mg/kg.
 CC Treatment with the oligopeptides increases the life of transplants
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 29; DB 2; Length 10;
 Best Local Similarity 40.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RXXXXXXGY 10
 Db 1 RLVRLLLGY 10

RESULT 9
 AAW82809
 ID AAW82809 standard; peptide; 10 AA.

XX
 AC AAW82809;

DT 28-JAN-1999 (first entry)

XX Cytomodulating lipophilic oligopeptide (f).

XX Cytomodulating lipophilic oligopeptide; immune system; inflammation;
 KW cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T cell;
 KW B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis;
 KW Crohn's disease; colitis; allergy; transplant.

XX Synthetic.

XX WO9846633-A1.

XX 22-OCT-1998.

XX 10-APR-1998; 98WO-US007231.

XX 11-APR-1997; 97US-00838916.

XX 23-FEB-1998; 98US-00028083.

XX (SANG-) SANGSTAT MEDICAL CORP.

XX Buelow R, Grassy G, Calas B;

XX WPI; 1998-594558/50.

XX New lipophilic peptide(s) that inhibit activation of immune system cells
 PT - used for, e.g. production of cytokine(s) and the inflammatory response,
 PT and also for modulating haem-containing enzymes.

XX Claim 7; Page 37; 48pp; English.

XX AAW82804 to AAW82829 are cytomodulating lipophilic oligopeptides. The
 CC oligopeptides are used to inhibit: (i) activity of lymphocytes
 CC (particularly cytotoxic T cells, but also natural killers, B cells and
 CC mononuclear phagocytes); (ii) production of inflammatory cytokines, and
 CC (iii) an inflammatory response in mammals (e.g. in cases of septic shock,
 CC rheumatoid arthritis (RA), Crohn's disease, colitis and allergy). They

CC are also used for modulating activity of haem-containing enzymes and for
 CC delaying onset of autoimmune disease (specifically insulin-dependent
 CC diabetes mellitus, RA and systemic lupus erythematosus). In all cases the
 CC oligopeptides may be generated from nucleic acids, and treatments are in
 CC vitro or in vivo. A specific application is treatment of organs or cells
 CC for transplantation, or of the recipient of such transplants. Apart from
 CC therapeutic use, the oligopeptides can be used to study mechanisms of T
 CC cell (de)activation and to raise antibodies (used to identify
 CC oligopeptides and to raise anti-idiotypic antibodies that are competitors
 CC of the oligopeptides). The oligopeptides are administered by bolus
 CC injection or infusion, typically at 0.1-50 (preferably 1-25) mg/kg.
 CC Treatment with the oligopeptides increases the life of transplants
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 29; DB 2; Length 10;
 Best Local Similarity 40.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RXXXXXXGY 10
 Db 1 RLVRLLLGY 10

RESULT 10
 AAW82822
 ID AAW82822 standard; peptide; 10 AA.

XX
 AC AAW82822;

DT 28-JAN-1999 (first entry)

XX Cytomodulating lipophilic oligopeptide (s).

XX Cytomodulating lipophilic oligopeptide; immune system; inflammation;
 KW cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T cell;
 KW B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis;
 KW Crohn's disease; colitis; allergy; transplant.

XX Synthetic.

XX WO9846633-A1.

XX 22-OCT-1998.

XX 10-APR-1998; 98WO-US007231.

XX 11-APR-1997; 97US-00838916.

XX 23-FEB-1998; 98US-00028083.

XX (SANG-) SANGSTAT MEDICAL CORP.

XX Buelow R, Grassy G, Calas B;

XX WPI; 1998-594558/50.

XX New lipophilic peptide(s) that inhibit activation of immune system cells
 PT - used for, e.g. production of cytokine(s) and the inflammatory response,
 PT and also for modulating haem-containing enzymes.

XX Claim 7; Page 37; 48pp; English.

XX AAW82804 to AAW82829 are cytomodulating lipophilic oligopeptides. The
 CC oligopeptides are used to inhibit: (i) activity of lymphocytes
 CC (particularly cytotoxic T cells, but also natural killers, B cells and
 CC mononuclear phagocytes); (ii) production of inflammatory cytokines, and
 CC (iii) an inflammatory response in mammals (e.g. in cases of septic shock,
 CC rheumatoid arthritis (RA), Crohn's disease, colitis and allergy). They
 CC are also used for modulating activity of haem-containing enzymes and for
 CC delaying onset of autoimmune disease (specifically insulin-dependent
 CC diabetes mellitus, RA and systemic lupus erythematosus). In all cases the
 CC oligopeptides may be generated from nucleic acids, and treatments are in
 CC vitro or in vivo. A specific application is treatment of organs or cells

CC for transplantation, or of the recipient of such transplants. Apart from
 CC therapeutic use, the oligopeptides can be used to study mechanisms of T
 CC cell (de)activation and to raise antibodies (used to identify
 CC oligopeptides and to raise anti-idiotypic antibodies that are competitors
 CC of the oligopeptides. The oligopeptides are administered by bolus
 CC injection or infusion, typically at 0.1-50 (preferably 1-25) mg/kg.
 CC Treatment with the oligopeptides increases the life of transplants
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 29; DB 2; Length 10;
 Best Local Similarity 40.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXXRXXXGY 10
 |::|::|
 Db 1 RLLRLWGY 10

RESULT 11
 AAW82811
 ID AAW82811 standard; peptide; 10 AA.
 XX
 AC AAW82811;

DT 28-JAN-1999 (first entry)

DE Cytomodulating lipophilic oligopeptide (h).

CC Cytomodulating lipophilic oligopeptide; immune system; inflammation;
 KW cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T cell;
 KW B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis;
 KW Crohn's disease; colitis; allergy; transplant.

XX Synthetic.

OS

PN WO9846633-A1.

XX 22-OCT-1998.

PF 10-APR-1998; 98WO-US007231.

PR 11-APR-1997; 97US-00838916.

PR 23-FEB-1998; 98US-00028083.

XX (SANG-) SANGSTAT MEDICAL CORP.

XX Buelow R, Grassy G, Calas B;

XX WPI; 1998-594558/50.

XX New lipophilic peptide(s) that inhibit activation of immune system cells

PT - used for, e.g. production of cytokine(s) and the inflammatory response,

PT and also for modulating haem-containing enzymes.

XX Claim 7; Page 37; 48pp; English.

XX AAW82804 to AAW82829 are cytomodulating lipophilic oligopeptides. The
 CC oligopeptides are used to inhibit: (i) activity of lymphocytes
 CC (particularly cytotoxic T cells, but also natural killers, B cells and
 CC mononuclear phagocytes); (ii) production of inflammatory cytokines, and
 CC (iii) an inflammatory response in mammals (e.g. in cases of septic shock,
 CC rheumatoid arthritis (RA), Crohn's disease, colitis and allergy). They
 CC are also used for modulating activity of haem-containing enzymes and for
 CC delaying onset of autoimmune disease (specifically insulin-dependent
 CC diabetes mellitus, RA and systemic lupus erythematosus). In all cases the
 CC oligopeptides may be generated from nucleic acids, and treatments are in
 CC vitro or in vivo. A specific application is treatment of organs or cells
 CC for transplantation, or of the recipient of such transplants. Apart from
 CC therapeutic use, the oligopeptides can be used to study mechanisms of T
 CC cell (de)activation and to raise antibodies (used to identify
 CC oligopeptides and to raise anti-idiotypic antibodies that are competitors
 CC of the oligopeptides. The oligopeptides are administered by bolus

CC injection or infusion, typically at 0.1-50 (preferably 1-25) mg/kg.
 CC Treatment with the oligopeptides increases the life of transplants
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 29; DB 2; Length 10;
 Best Local Similarity 40.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXXRXXXGY 10
 |::|::|
 Db 1 RLLRLVGY 10

RESULT 12
 AAW82816
 ID AAW82816 standard; peptide; 10 AA.
 XX
 AC AAW82816;

DT 28-JAN-1999 (first entry)

DE Cytomodulating lipophilic oligopeptide (m).

CC Cytomodulating lipophilic oligopeptide; immune system; inflammation;
 KW cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T cell;
 KW B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis;
 KW Crohn's disease; colitis; allergy; transplant.

XX Synthetic.

OS

PN WO9846633-A1.

XX 22-OCT-1998.

PF 10-APR-1998; 98WO-US007231.

PR 11-APR-1997; 97US-00838916.

PR 23-FEB-1998; 98US-00028083.

XX (SANG-) SANGSTAT MEDICAL CORP.

XX Buelow R, Grassy G, Calas B;

XX WPI; 1998-594558/50.

XX New lipophilic peptide(s) that inhibit activation of immune system cells

PT - used for, e.g. production of cytokine(s) and the inflammatory response,

PT and also for modulating haem-containing enzymes.

XX Claim 7; Page 37; 48pp; English.

XX AAW82804 to AAW82829 are cytomodulating lipophilic oligopeptides. The
 CC oligopeptides are used to inhibit: (i) activity of lymphocytes
 CC (particularly cytotoxic T cells, but also natural killers, B cells and
 CC mononuclear phagocytes); (ii) production of inflammatory cytokines, and
 CC (iii) an inflammatory response in mammals (e.g. in cases of septic shock,
 CC rheumatoid arthritis (RA), Crohn's disease, colitis and allergy). They
 CC are also used for modulating activity of haem-containing enzymes and for
 CC delaying onset of autoimmune disease (specifically insulin-dependent
 CC diabetes mellitus, RA and systemic lupus erythematosus). In all cases the
 CC oligopeptides may be generated from nucleic acids, and treatments are in
 CC vitro or in vivo. A specific application is treatment of organs or cells
 CC for transplantation, or of the recipient of such transplants. Apart from
 CC therapeutic use, the oligopeptides can be used to study mechanisms of T
 CC cell (de)activation and to raise antibodies (used to identify
 CC oligopeptides and to raise anti-idiotypic antibodies that are competitors
 CC of the oligopeptides. The oligopeptides are administered by bolus
 CC injection or infusion, typically at 0.1-50 (preferably 1-25) mg/kg.
 CC Treatment with the oligopeptides increases the life of transplants
 XX
 SQ Sequence 10 AA;

```
Query Match      100.0%; Score 29; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXXXXXGY 10
    |::|::|
Db 1 RLLRLVLYG 10

RESULT 13
AAW82820
ID AAW82820 standard; peptide; 10 AA.
XX
AC AAW82820;
XX
DT 28-JAN-1999 (first entry)
XX
DE Cytomodulating lipophilic oligopeptide (q).
XX
KW Cytomodulating lipophilic oligopeptide; immune system; inflammation;
KW cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T cell;
KW B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis;
KW Crohn's disease; colitis; allergy; transplant.
XX
OS Synthetic.
XX
PN WO9846633-A1.
XX
PD 22-OCT-1998.
XX
PF 10-APR-1998; 98WO-US007231.
XX
PR 11-APR-1997; 97US-00838916.
PR 23-FEB-1998; 98US-00028083.
XX
PA (SANG-) SANGSTAT MEDICAL CORP.
XX
PI Buelow R, Grassy G, Calas B;
XX
DR WPI; 1998-594558/50.
XX
PT New lipophilic peptide(s) that inhibit activation of immune system cells
PT - used for, e.g. production of cytokine(s) and the inflammatory response,
PT and also for modulating haem-containing enzymes.
XX
PS Claim 7; Page 37; 48pp; English.
XX
CC AAW82804 to AAW82829 are cytomodulating lipophilic oligopeptides. The
CC oligopeptides are used to inhibit: (i) activity of lymphocytes
CC (particularly cytotoxic T cells, but also natural killers, B cells and
CC mononuclear phagocytes); (ii) production of inflammatory cytokines, and
CC (iii) an inflammatory response in mammals (e.g. in cases of septic shock,
CC rheumatoid arthritis (RA), Crohn's disease, colitis and allergy). They
CC are also used for modulating activity of haem-containing enzymes and for
CC delaying onset of autoimmune disease (specifically insulin-dependent
CC diabetes mellitus, RA and systemic lupus erythematosus). In all cases the
CC oligopeptides may be generated from nucleic acids, and treatments are in
CC vitro or in vivo. A specific application is treatment of organs or cells
CC for transplantation, or of the recipient of such transplants. Apart from
CC therapeutic use, the oligopeptides can be used to study mechanisms of T
CC cell (de)activation and to raise antibodies (used to identify
CC of the oligopeptides). The oligopeptides are administered by bolus
CC injection or infusion, typically at 0.1-50 (preferably 1-25) mg/kg.
CC Treatment with the oligopeptides increases the life of transplants
XX
SQ Sequence 10 AA;

Query Match      100.0%; Score 29; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXXXXXGY 10
    |::|::|
Db 1 RLLRLVLYG 10

RESULT 15
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Db 1 RLLRLVLYG 10
    |::|::|

RESULT 14
AAW82827
ID AAW82827 standard; peptide; 10 AA.
XX
AC AAW82827;
XX
DT 28-JAN-1999 (first entry)
XX
DE Cytomodulating lipophilic oligopeptide (x).
XX
KW Cytomodulating lipophilic oligopeptide; immune system; inflammation;
KW cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T cell;
KW B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis;
KW Crohn's disease; colitis; allergy; transplant.
XX
OS Synthetic.
XX
PN WO9846633-A1.
XX
PD 22-OCT-1998.
XX
PF 10-APR-1998; 98WO-US007231.
XX
PR 11-APR-1997; 97US-00838916.
PR 23-FEB-1998; 98US-00028083.
XX
PA (SANG-) SANGSTAT MEDICAL CORP.
XX
PI Buelow R, Grassy G, Calas B;
XX
DR WPI; 1998-594558/50.
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CC of the oligopeptides). The oligopeptides are administered by bolus
CC injection or infusion, typically at 0.1-50 (preferably 1-25) mg/kg.
CC Treatment with the oligopeptides increases the life of transplants
XX
SQ Sequence 10 AA;

Query Match      100.0%; Score 29; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXXXXXGY 10
    |::|::|
Db 1 RLLRLVLYG 10

RESULT 15
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AAW82821
 ID AAW82821 standard; peptide; 10 AA.
 XX
 AC AAW82821;
 XX
 DT 28-JAN-1999 (first entry)
 XX
 DE Cytomodulating lipophilic oligopeptide (r).
 XX
 KW Cytomodulating lipophilic oligopeptide; immune system; inflammation;
 KW cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T cell;
 KW B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis;
 KW Crohn's disease; colitis; allergy; transplant.
 XX
 OS Synthetic.
 XX
 PN WO9846633-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 10-APR-1998; 98WO-US007231.
 XX
 PR 11-APR-1997; 97US-00838916.
 PR 23-FEB-1998; 98US-00028083.
 XX
 PA (SANG-) SANGSTAT MEDICAL CORP.
 XX
 PI Buelow R, Grassay G, Calas B;
 XX
 DR WPI; 1998-594558/50.
 XX
 PT New lipophilic peptide(s) that inhibit activation of immune system cells
 PT - used for, e.g. production of cytokine(s) and the inflammatory response,
 PT and also for modulating haem-containing enzymes.
 XX
 PS Claim 7; Page 37; 48pp; English.
 XX
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 CC delaying onset of autoimmune disease (specifically insulin-dependent
 CC diabetes mellitus, RA and systemic lupus erythematosus). In all cases the
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 CC therapeutic use, the oligopeptides can be used to study mechanisms of T
 CC cell (de)activation and to raise antibodies (used to identify
 CC oligopeptides and to raise anti-idiotypic antibodies that are competitors
 CC of the oligopeptides. The oligopeptides are administered by bolus
 CC injection or infusion, typically at 0.1-50 (preferably 1-25) mg/kg.
 CC Treatment with the oligopeptides increases the life of transplants
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 29; DB 2; Length 10;
 Best Local Similarity 40.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RXXRXXXGY 10
 Db |:::|:::|
 1 RLRLRLWLY 10

Search completed: February 1, 2005, 06:57:23
 Job time : 67 secs